

SEQUENCE LISTING

<110> BANYU PHARMACEUTICAL CO., LTD.

<120> NOVEL GUANOSINE TRIPHOSPHATE (GTP) BINDING PROTEIN-COUPLED RECEPTOR
PROTEINS

<130> B1-103PCT

<140>

<141>

<150> PCT/JP98/05967

<151> 1998-12-25

<150> JP 1999-145661

<151> 1999-05-25

<160> 26

<170> PatentIn Ver. 2.0

<210> 1

<211> 413

<212> PRT

<213> Rattus norvegicus

<400> 1

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu
 1 5 10 15

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
 20 25 30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 35 40 45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
 50 55 60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
 85 90 95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val
 100 105 110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115	120	125	
Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala			
130	135	140	
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp			
145	150	155	160
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr			
165	170	175	
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe			
180	185	190	
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe			
195	200	205	
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn			
210	215	220	
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly			
225	230	235	240
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro			
245	250	255	

Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu

260

265

270

His Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

275

280

285

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

290

295

300

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

305

310

315

320

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

325

330

335

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

340

345

350

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

355

360

365

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

370

375

380

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

385

390

395

400

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

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<210> 2

<211> 1239

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(1239)

<400> 2

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Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1 5 10 15

gcc gga gag gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc 96

Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca 144

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

gta	c _{tg}	g _{gc}	a _{ac}	g _{cg}	c _{tg}	g _{tc}	a _{tg}	c _{tc}	g _{cc}	t _{tc}	g _{tg}	g _{cg}	g _{at}	t _{cg}	a _{gc}	192
Val	Leu	Gly	Asn	Ala	Leu	Val	Met	Leu	Ala	Phe	Val	Ala	Asp	Ser	Ser	
	50			55				60								
c _{tc}	c _{gc}	a _{cc}	c _{ag}	a _{ac}	a _{ac}	t _{tc}	t _{tt}	c _{tg}	c _{tc}	a _{ac}	c _{tc}	g _{cc}	a _{tc}	t _{cc}	g _{ac}	240
Leu	Arg	Thr	Gln	Asn	Asn	Phe	Phe	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	
	65			70				75				80				
t _{tc}	c _{tc}	g _{tg}	g _{gt}	g _{cc}	t _{tc}	t _{gc}	a _{tc}	c _{ca}	t _{tg}	t _{ac}	g _{ta}	c _{cc}	t _{at}	g _{tg}	c _{tg}	288
Phe	Leu	Val	Gly	Ala	Phe	Cys	Ile	Pro	Leu	Tyr	Val	Pro	Tyr	Val	Leu	
	85			90				95								
a _{cc}	g _{gc}	c _{gt}	t _{gg}	a _{cc}	t _{tc}	g _{gc}	c _{gg}	g _{gc}	c _{tc}	t _{gc}	a _{ag}	c _{tg}	t _{gg}	c _{tg}	g _{tg}	336
Thr	Gly	Arg	Trp	Thr	Phe	Gly	Arg	Gly	Leu	Cys	Lys	Leu	Trp	Leu	Val	
	100			105				110								
g _{ta}	g _{ac}	t _{ac}	c _{ta}	c _{tg}	t _{gt}	g _{cc}	t _{cc}	t _{cg}	g _{tc}	t _{tc}	a _{ac}	a _{tc}	g _{ta}	c _{tc}	a _{tc}	384
Val	Asp	Tyr	Leu	Leu	Cys	Ala	Ser	Ser	Val	Phe	Asn	Ile	Val	Leu	Ile	
	115			120				125								
a _{gc}	t _{at}	g _{ac}	c _{ga}	t _{tc}	c _{tg}	t _{ca}	g _{tc}	a _{ct}	c _{ga}	g _{ct}	g _{tc}	t _{cc}	t _{ac}	agg	g _{cc}	432
Ser	Tyr	Asp	Arg	Phe	Leu	Ser	Val	Thr	Arg	Ala	Val	Ser	Tyr	Arg	Ala	
	130			135				140								
c _{ag}	c _{ag}	g _{gg}	g _{ac}	a _{cg}	a _{ga}	c _{gg}	g _{cc}	g _{tt}	c _{gg}	a _{ag}	a _{tg}	g _{ca}	c _{tg}	g _{tg}	t _{gg}	480

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145

150

155

160

gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac 528

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc 576

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc 624

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac 672

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc 720

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly

225

230

235

240

cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc 768

Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro

245

250

255

agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg	816		
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Glu Ala Met Pro Leu			
260	265	270	
cac agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc	864		
His Ser Ser Gly Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu			
275	280	285	
aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc	912		
Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg			
290	295	300	
atg aag atg gig tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg	960		
Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg			
305	310	315	320
gac aag aag gtg gcc aag tcg ctg gcc atc atc gtg agc atc ttt ggg	1008		
Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly			
325	330	335	
ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc	1056		
Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys			
340	345	350	
cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt	1104		

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

355

360

365

ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1152

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

370

375

380

tac agc ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc 1200

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

385

390

395

400

aag gtc cag ccc cac ggc tcc ctg gag cag tgc tgg aag 1239

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

405

410

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 3

batngccaaac ctbkcccttct c

21

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 4

ccataaaagn ngggttigac

20

<210> 5

<211> 2700

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (351)..(1589)

<400> 5

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accgacgcac cgcgggcggc tggagctcgg ctttgccttc gctgcagcag ccgcgcggcc 120

cgccccactc cgctcagatt ccgacaccag cccccctctgg atcgccctcc tggactctag 180

cccggtctct tgcctccgacc ccgcggacca tgctccggc gccccccgga aaaccgggt 240

gggcgaagag ccggcaaaga ttaggctcac gagcggggc cccacccggc caccaggctc 300

tccgcggcgg ccctgcccgg tgcctccgag ccgtgtgagc ctgcgtggcc atg gag 356

Met Glu

1

cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg gcc gga 404

Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu Ala Gly

5

10

15

gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc tgg acc 452

Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr

20

25

30

gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca gta ctg 500

Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr Val Leu

35

40

45

50

ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc ctc cgc 548

Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser Leu Arg

55

60

65

acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac ttc ctc 596

Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu

70

75

80

gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg acc ggc 644

Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly

85

90

95

cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg tgg ctg gtg gta gac 692

Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val Val Asp

100

105

110

tac cta ctg tgt gcc tcc tcg gtc ttc aac atc gta ctc atc agc tat 740

Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile Ser Tyr

115

120

125

130

gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc cag cag 788

Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln

135

140

145

ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gtg tgg gtg ctg 836

Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp Val Leu

150

155

160

gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac ctg tct 884

Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser

165

170

175

ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc ttc tac 932

Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr

180

185

190

aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc acg ccc 980

Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro

195

200

205

210

ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac atc cag 1028

Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln

215

220

225

agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc cca gaa 1076

Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly Pro Glu

230

235

240

ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc agc tgc 1124

Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro Ser Cys

245

250

255

tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg cac agc 1172

Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu His Ser

260

265

270

tct	ggc	agc	tcc	tca	agg	ggc	act	gag	agg	cca	cgc	tca	ctc	aaa	agg	1220
Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg																
275			280				285					290				
ggc	tcc	aag	cca	tca	gca	tct	tca	gca	tcc	ctg	gag	aag	cgc	atg	aag	1268
Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg Met Lys																
		295					300					305				
atg	gig	tcc	cag	agc	atc	acc	cag	cgc	ttc	cgg	ctg	tcg	cgg	gac	aag	1316
Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg Asp Lys																
		310				315						320				
aag	gtg	gcc	aag	tcg	ctg	gcc	atc	atc	gtg	agc	atc	ttt	ggg	ctc	tgc	1364
Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly Leu Cys																
		325			330							335				
tgg	gcf	ccg	tac	acg	ctc	ctc	atg	atc	atc	cga	gct	gct	tgc	cat	ggc	1412
Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys His Gly																
		340			345							350				
cgc	tgc	atc	ccc	gat	tac	tgg	tac	gag	acg	tcc	ttc	tgg	ctt	ctg	tgg	1460
Arg Cys Ile Pro Asp Tyr Trp TyrGlu Thr Ser Phe Trp Leu Leu Trp																
		355			360							365			370	
gcc	aac	tcg	gcc	gtc	aac	ccc	gtc	ctc	tac	cca	ctg	tgc	cac	tac	agc	1508

Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His Tyr Ser

375

380

385

ttc cgc aga gcc ttc acc aag ctc ctc tgc ccc cag aag ctc aag gtc 1556

Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu Lys Val

390

395

400

cag ccc cac ggc tcc ctg gag cag tgc tgg aag tggcggctg cccacccctt 1609

Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

405

410

ctgaggccag gcccttgcac ttgtttgagt gggcagccgg agcgttggcg gggcccttgtt 1669

ccatgcctcg ctccaaatgc catggcggcc tcttagatca tcaacccgc agtgggttag 1729

catggcaggtt gggccaagag cccttagttgg tggagctaga gtgtgttgtt tagctctgcc 1789

gccacattct ctttaccac acagaagaga caatccagga gtccaggca tgccttccac 1849

ctacacacac acacacacac acacacacac acacaccaca gtgtgtgttcc agtgtatgtcc 1909

ccctttgtcat atttagtgtt tgggtgtccctc cctaaatgcaa acctcggtgtt gtgtttccgg 1969

ctccggccct ggcaatgcgt gcgtgcgccc tgcattgtgtt cacacccggc acacacccgc 2029

ccggccacaca citgcaacac ctccctcttc ccagaagagc tggggacgtt gcccatttgtt 2089

gccactgtct ctigcttaat cccagagcct ggctccctat cccccactct cccttcaact 2149
ctgccccaca aagtgtcgag cgccctcggga aacttgaagc ttctctgctc ctccactct 2209
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aaaaaaaaaaa a 2700

<210> 6

〈211〉 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 6

cgaggatccg tgggtccg gggccgtc

29

<210> 7

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 7

cggtaagct tcacgacacc tggaaatggaa ga

32

<210> 8

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 8

ccttctgcat cccattgtac gtacc

24

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 9

cttccggccgg gccttacacca a

21

<210> 10

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 10

acagacacgg cggggctcac

20

<210> 11

<211> 1350

<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (280)..(557)

<400> 11

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ctcctctcccc gctgcagcag ccgcgtgccc ggccccacig ggctcggatc cggcccccggc 120

cccctcggca ccgcgtgcic tggcccccggc cccggccccc cggaccatgc gctggcggcc 180

cccaggggaa cccgacccgg ccaagggccc gcaaagacga ggctcccgaa ccggggcccc 240

tcccgccgc ccagctctcg gccggcgccc tggcccgct cccggagccg cgtgagccctg 300

cgggggccatg gagcgcgcgc cgcccgacgg gccgcgtgaac gcttcggggg cgctggcggg 360

cgaggcggcg gcggcgggcg gggcgcgccg cttcicggca gcctggaccg cggtgciggc 420

cgcgcicatg ggcgtgcaca tcgtggccac ggtgcgtggc aacgcgtgg tcatgcicgc 480

tttcgtggcc gactcgagcc tccgcaccca gaacaacttc ttccgtcaca acctcgccc 540

ciccgacttc ctgcgtcggt aatccccagc ccctggccgc tggggaccca ggggcgccc 600

gcgtggccgg gccagcgggg actggaacac ggacctgggt ggctccgcgca ggcacacgcc 660

ccaccagggg acccgccctg ggaagggggc gicccggagcc catgggtgg ggggcacagg 720

cgaaggttct tgccacttag gcctcggtac agggctggg gagagaatgtc cccgggaagg 780

gacacgggca ctggcgagg cgcaaggcgc aaaggcagcg ggigcagctc tggctcctgc 840

gctgttagcca aacaaaggct gctgcggact taggacgcgc ggagggcgca gttggggcggt 900

tttagagaagg tctggggag gggacatgga agggggattt tttagagcgt gttggggaa 960

gggacggigg ggaagggtggg ggttggggga gacgcgtcgga ggagcgtgt ctcacgtgtc 1020

caggctctgc tgccggctgg gggcggggc acgcggagg ggctggagcg ccagacacct 1080

gttggggctg tgaggtggcgt ctcccaagacg ctcggcc 1140

gctggcggct ggcggctgca accaagtgcc ctttcagccg ggagaaaaggc tttttccttg 1200

tctaaggctg a gaccggagggti tgicccagcgc cagggttaggg gcggatggatcc agcggggggag 1260

gggagaagga aatgtcttc ttccctcctt tgagggctgg gagggctgga cagaagtcca 1320

gggaatcccc acicccaggct ctcggggggc 1350

<210> 12

〈211〉 448

<212> DNA

<213> *Homo sapiens*

〈220〉

<221> exon

$\langle 222 \rangle$ (259) .. (425)

〈400〉 12

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aggggtggta agaigaggat ggctagttcc agaaaagcag ccaccaatgtg accccaggtc 180

ccgcccggtgt ctgcgccttag gtccgtctgt cccctggccc ctggctgcat ggtcccaactg 240

tggccctact ccccacaggc gccttctgca tcccactgia tgtaccctac gtgcgtacag 300

gccgciggac cttcgccgg ggcctctgca agctgiggct ggttagiggac tacctgctgt 360

gcaccctccctc tgccttcaac atcggtgtca ttagctacga ccgccttccctg tcggcaccc 420

gagcggigag tccatggctg cggagctc 448

<210> 13

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<212> DNA

<213> Homo sapiens

<220>

<221> exon

<222> (293)..(1209)

<400> 13

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agtggggagg gitagaggaa gggagggaa agagggaggg agggaggaca ggagggaaa 180

ggaggagcat tgctgctgag ggaagggccc acatagggc ccacaggcta cggggcgca 240

cccgcccaa tattccttcc gcccccccccc tgaccagcct gcccttctgc aggtctcata 300

ccgggcccag cagggtgaca cgcggcggc agtgcggaag atgcgtgtgg tgigggtgt 360

ggcccttcctg ctgtacggac cagccatcct gagctggag tacctgtccg gggcagc 420

catccccgag ggccactgct aigccgagtt ctcttacaac tggtacttcc tcatcacggc 480

ttccaccctg gagttttttt cgccttcct cagcgtcacc ttcttiaacc tcagcatcta 540

cctgaacatc cagaggcgca cccgcctccg gctggatggg gctcgagagg cagccggccc 600

cgagccccct cccgaggccc agccctcacc acccccacccg cctggtgtgct gggctgtg 660

gcagaagggg cacggggagg ccatgccgt gcacaggtaat ggggtgggtgg aggccggcgt 720

aggcgctgag gccggggagg cgaccctcgg gggtgtggcggt gggggcggct ccgtggcttc 780

acccacccctcc agctccggca gctccctcgag gggcactgag aggccgcgt cactcaagag 840

gggcctccaag ccatcggcgt cctcgccctc actggagaag cgcatgaaga tggtgtccca 900

gagcttccacc cagcgcittc ggctgtctcg ggacaggaaa gtggccaagt cgctggccgt 960

catcggtggc atctttgggc tctgctgggc cccatacagc ctgtgtatga tcatccgggc 1020

cgccctggccat ggccacttgtcg tccccgtacta cgggtacgaa accttccttctt ggcctccgtgt 1080

ggccaactcg gcttgtcaacc ctgtccctta cccctgtgtgc caccacagct tccggccgggc 1140

cttcaccaag ctgcctctgcc cccagaagct caaaatccag ccccacagct cccctggagca 1200

ctgciggaag tgagtggccc accagagcct cccctcagccca cgcctcttc agcccgaggtc 1260

icctggccat ctggccctgc tgccccctac ccggctcggt ccccccagggg tgagccccgc 1320

cgtgtctgtg gcctctctt aatgccacgg cagccacccctt gccaaaggagg cgccttcctg 1380

gggtggccag agggccccctc actgtgcgttga cttggaggcttg gtgtggccggc cctgtcccccc 1440

acattctggc tccacccggga gggacagtc t ggaggtcccc a gacatgc tgc ccaccccttg 1500

ctgggtggccca cccttgcgca gttaciggttg gttgttcttcc caaaggcaaggc accttgggtgt 1560

gctccaggcttcctggccatgcaggttggcttcgtgcacgtgcacacaccgtgcacacccctgt 1620

ctgtctcttg cataaggcctc aggcctggcc ctttcacccc tcttcccacc aacictct 1740

gcccccaaaa gtgtcaaggg gcccttaggaa cctcgaagct gtgtctgtct tttccattct 1800

gggtgttttc agaaagaiga agaagaaaac atgictgtga acttgatgtt cctgggaigt 1860

ttaatcaaga gagacaaaat tgctgaggag ctc 1893

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 14

tgaacgcctc gggggcgctg 20

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 15

gagatggcga ggttgagcag g

21

<210> 16

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 16

ggctccaaggc catcggtcg

20

<210> 17

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially

synthesized primer sequence

<400> 17

ctcacitcca gcagtgctcc

20

<210> 18

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 18

gcctccgcac ccagaacaac

20

<210> 19

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially
synthesized primer sequence

<400> 19

tgcgccctcg gatgttcag

19

<210> 20

<211> 453

<212> PRT

<213> Homo sapiens

<400> 20

Met Glu Arg Ala Pro Pro Asp Gly Pro Leu Asn Ala Ser Gly Ala Leu
 1 5 10 15

Ala Gly Glu Ala Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala
 20 25 30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr
 35 40 45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser
 50 55 60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu
 85 90 95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100

105

110

Val Asp Tyr Leu Leu Cys Thr Ser Ser Ala Phe Asn Ile Val Leu Ile

115

120

125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Leu Leu Val Trp

145

150

155

160

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195

200

205

Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn

210

215

220

Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Ala Arg Glu Ala Ala

225 230 235 240

Gly Pro Glu Pro Pro Pro Glu Ala Gln Pro Ser Pro Pro Pro Pro

245 250 255

Gly Cys Trp Gly Cys Trp Gln Lys Gly His Gly Glu Ala Met Pro Leu

260 265 - 270

His Arg Tyr Gly Val Gly Glu Ala Ala Val Gly Ala Glu Ala Gly Glu

275 280 285

Ala Thr Leu Gly Gly Gly Gly Gly Ser Val Ala Ser Pro Thr

290 295 300

Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

305 310 315 320

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

325 330 335

Met Lys Met Val Ser Gln Ser Phe Thr Gln Arg Phe Arg Leu Ser Arg

340 345 350

Asp Arg Lys Val Ala Lys Ser Leu Ala Val Ile Val Ser Ile Phe Gly

355 360 365

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

370

375

380

His Gly His Cys Val Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

385

390

395

400

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

His Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

Lys Ile Gln Pro His Ser Ser Leu Glu His Cys Trp Lys Lys Met Lys

435

440

445

Lys Lys Thr Cys Leu

450

<210> 21

<211> 2050

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (271)..(1629)

<400> 21

agagatgttag ggcgc(ccc)tt ttagctgcgc acagaacgaa agaactcg(ttt)ttttaa 60

gtgagtgigc tgggtgacg cttagggcgc cctccgcagt gcgcgcagga aagcgcactg 120

aggctgcgga ggcagagctg catgctgggt gcgggaagag gtgggc(cc)tcgcggagtc 180

gctgagtcgg tgccctttta gtttagttctg cagtctagta tggtccccat tggcccttcc 240

actccggag ccgcgtgagc ctgcggggcc atg gag cgc gcg ccg ccc gac ggg 294

Met Glu Arg Ala Pro Pro Asp Gly

1 5

ccg ctg aac gct tcg ggg gcg ctg gcg ggc gag gcg gcg gcg ggc 342

Pro Leu Asn Ala Ser Gly Ala Leu Ala Gly Glu Ala Ala Ala Ala Gly

10 15 20

ggg gcg cgc ggc ttc tcg gca gcc tgg acc gcg gtg ctg gcc gcg ctc 390

Gly Ala Arg Gly Phe Ser Ala Ala Trp Thr Ala Val Leu Ala Ala Leu

25 30 35 40

atg gcg ctg ctc atc gtg gcc acg gtg ctg ggc aac gcg ctg gtc atg 438

Met Ala Leu Leu Ile Val Ala Thr Val Leu Gly Asn Ala Leu Val Met

45 50 55

ctc gcc ttc gtg gcc gac tcg agc ctc cgc acc cag aac aac ttc ttc 486
 Leu Ala Phe Val Ala Asp Ser Ser Leu Arg Thr Gln Asn Asn Phe Phe
 60 65 70

ctg ctc aac ctc gcc atc tcc gac ttc ctc gtc ggc gcc ttc tgc atc 534
 Leu Leu Asn Leu Ala Ile Ser Asp Phe Leu Val Gly Ala Phe Cys Ile
 75 80 85

cca ctg tat gta ccc tac gtg ctg aca ggc cgc tgg acc ttc ggc cgg 582
 Pro Leu Tyr Val Pro Tyr Val Leu Thr Gly Arg Trp Thr Phe Gly Arg
 90 95 100

ggc ctc tgc aag ctg tgg ctg gta gtg gac tac ctg ctg tgc acc tcc 630
 Gly Leu Cys Lys Leu Trp Leu Val Val Asp Tyr Leu Leu Cys Thr Ser
 105 110 115 120

tct gcc ttc aac atc gtg ctc atc agc tac gac cgc ttc ctg tcg gtc 678
 Ser Ala Phe Asn Ile Val Leu Ile Ser Tyr Asp Arg Phe Leu Ser Val
 125 130 135

acc cga gcg gtc tca tac cgg gcc cag cag ggt gac acg cgg cgg gca 726
 Thr Arg Ala Val Ser Tyr Arg Ala Gln Gln Gly Asp Thr Arg Arg Ala
 140 145 150

gtg cgg aag atg ctg ctg gtg tgg gtg ctg gcc ttc ctg ctg tac gga 774
 Val Arg Lys Met Leu Leu Val Trp Val Leu Ala Phe Leu Leu Tyr Gly

155	160	165
cca gcc atc ctg agc tgg gag tac ctg tcc ggg ggc agc tcc atc ccc		
Pro Ala Ile Leu Ser Trp Glu Tyr Leu Ser Gly Gly Ser Ser Ile Pro		
170	175	180
gag ggc cac tgc tat gcc gag ttc ttc tac aac tgg tac ttc ctc atc		
Glu Gly His Cys Tyr Ala Glu Phe Phe Tyr Asn Trp Tyr Phe Leu Ile		
185	190	195
195		
acg gct tcc acc ctg gag ttc ttt acg ccc ttc ctc agc gtc acc ttc		
Thr Ala Ser Thr Leu Glu Phe Phe Thr Pro Phe Leu Ser Val Thr Phe		
205	210	215
215		
ttt aac ctc agc atc tac ctg aac atc cag agg cgc acc cgc ctc cgg		
Phe Asn Leu Ser Ile Tyr Leu Asn Ile Gln Arg Arg Thr Arg Leu Arg		
220	225	230
230		
ctg gat ggg gct cga gag gca gcc ggc ccc gag ccc cct ccc gag gcc		
Leu Asp Gly Ala Arg Glu Ala Ala Gly Pro Glu Pro Pro Glu Ala		
235	240	245
245		
cag ccc tca cca ccc cca ccg cct ggc tgc tgg ggc tgc tgg cag aag		
Gln Pro Ser Pro Pro Pro Pro Gly Cys Trp Gly Cys Trp Gln Lys		
250	255	260
260		

ggg cac ggg gag gcc atg ccg ctg cac agg tat ggg gtg ggt gag gcg 1110

Gly His Gly Glu Ala Met Pro Leu His Arg Tyr Gly Val Gly Glu Ala

265 270 275 280

gcc gta ggc gct gag gcc ggg gag gcg acc ctc ggg ggt ggc ggt ggg 1158

Ala Val Gly Ala Glu Ala Gly Glu Ala Thr Leu Gly Gly Gly Gly

285 290 295

ggc ggc tcc gig gct tca ccc acc tcc agc tcc ggc agc tcc tcg agg 1206

Gly Gly Ser Val Ala Ser Pro Thr Ser Ser Ser Gly Ser Ser Ser Arg

300 305 310

ggc act gag agg ccg cgc tca ctc aag agg ggc tcc aag ccg tcg gcg 1254

Gly Thr Glu Arg Pro Arg Ser Leu Lys Arg Gly Ser Lys Pro Ser Ala

315 320 325

tcc tcg gcc tcg ctg gag aag cgc aig aag atg gtg tcc cag agc ttc 1302

Ser Ser Ala Ser Leu Glu Lys Arg Met Lys Met Val Ser Gln Ser Phe

330 335 340

acc cag cgc ttt cgg ctg tct cgg gac agg aaa gtg gcc aag tcg ctg 1350

Thr Gln Arg Phe Arg Leu Ser Arg Asp Arg Lys Val Ala Lys Ser Leu

345 350 355 360

gcc gtc atc gtg agc atc ttt ggg ctc tgc tgg gcc cca tac acg ctg 1398

Ala Val Ile Val Ser Ile Phe Gly Leu Cys Trp Ala Pro Tyr Thr Leu

365	370	375
<pre> ctg atg atc aic cgg gcc tgc cat ggc cac tgc gtc cct gac tac 1446 Leu Met Ile Ile Arg Ala Ala Cys His Gly His Cys Val Pro Asp Tyr </pre>		
380	385	390
<pre> tgg tac gaa acc tcc ttc tgg ctc ctg tgg gcc aac tcg gct gtc aac 1494 Trp Tyr Glu Thr Ser Phe Trp Leu Leu Trp Ala Asn Ser Ala Val Asn </pre>		
395	400	405
<pre> cct gtc ctc tac cct ctg tgc cac cac agc ttc cgc cgg gcc ttc acc 1542 Pro Val Leu Tyr Pro Leu Cys His His Ser Phe Arg Arg Ala Phe Thr </pre>		
410	415	420
<pre> aag ctg ctc tgc ccc cag aag ctc aaa atc cag ccc cac agc tcc ctg 1590 Lys Leu Leu Cys Pro Gln Lys Leu Lys Ile Gln Pro His Ser Ser Leu </pre>		
425	430	435
<pre> gag cac tgc tgg aaa aag atg aag aag aaa aca tgc tgc tgg 1639 Glu His Cys Trp Lys Lys Met Lys Lys Lys Thr Cys Leu </pre>		
445	450	
<pre> gttccatggaa tggatataatca agagagacaa aatggatggag gagctcaggc ctggatggc 1699 aggatgtggcc tcccacggcc tcctccctcc gcttggctt ccggctggc tggccatgt 1759 </pre>		

gcttctgccc accccgcctc tgggctcaca ccagccctgg tggccaagcc tgccccggcc 1819

actctgttttgc ttcacccagg acctctgggg gtgttgttggga ggagggggcc cggctgggcc 1879

cgaggggtccc aaggcgigca ggggcggtcc agaggagggt cccgggcagg ggccgcitcg 1939

ccatgtgcig tgcacccggc ccacgcgcic tgcacgtcc tctgcctgtgc cccgcgtgcgc 1999

tgccttgcgaa accgttgggtt cacaataaaag tttttttttt tatttgttgcgtt g 2050

<210> 22

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 22

tgcatccat tgtacgttcc 20

<210> 23

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 23

atcattagga gcgtgtangg

20

<210> 24

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially synthesized primer sequence

<400> 24

tgcctctggga caccatcttc

20

<210> 25

<211> 445

<212> PRT

<213> Rattus norvegicus

<400> 25

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1 5 10 15

Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20 25 30

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35 40 45

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50 55 60

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65 70 75 80

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85 90 95

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100 105 110

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115 120 125

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130 135 140
Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp
145 150 155 160
Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr
165 170 175
Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe
180 185 190
Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe
195 200 205
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn
210 215 220
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly
225 230 235 240
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro
245 250 255
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu
260 265 270

His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu

275

280

285

Ala Ala Leu Gly Gly Ser Gly Gly Ala Ala Ala Ser Pro Thr

290

295

300

Ser Ser Ser Gly Ser Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu

305

310

315

320

Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg

325

330

335

Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg

340

345

350

Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly

355

360

365

Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys

370

375

380

His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu

385

390

395

400

Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

405

410

415

Tyr Ser Phe Arg Arg Ala Phe Thr Lys Leu Leu Cys Pro Gln Lys Leu

420

425

430

Lys Val Gln Pro His Gly Ser Leu Glu Gln Cys Trp Lys

435

440

445

<210> 26

<211> 1953

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (302)..(1636)

<400> 26

agcttaggggt gcaccgacgc accgcggcgg ctggagctcg gcittgcct cgctgcagca 60

gccccggccgc cccgccccact ccgcctcagat tccgacacca gccccctctg gatcgccctc 120

ctggacatctt gccccggcctc ttgcctccgac cccgcggacc atgcctccggg cgccccccgg 180

aaaaccgggc tgggcgaaga gccggcaaag attaggctca cgagcggggg ccccacccgg 240

ccacccagct ctccgccccgt gcccgtccccg gtgtccccga gccgtgtggag cctgctggc 300

c atg gag cgc gcg ccg ccc gac ggg ctg atg aac gcg tcg ggc act ctg 349

Met Glu Arg Ala Pro Pro Asp Gly Leu Met Asn Ala Ser Gly Thr Leu

1

5

10

15

gcc gga gag gcg gcg gct gca ggc ggg gcg cgc ggc ttc tcg gct gcc 397

Ala Gly Glu Ala Ala Ala Gly Gly Ala Arg Gly Phe Ser Ala Ala

20

25

30

tgg acc gct gtc ctg gct gcg ctc atg gcg ctg ctc atc gtg gcc aca 445

Trp Thr Ala Val Leu Ala Ala Leu Met Ala Leu Leu Ile Val Ala Thr

35

40

45

gta ctg ggc aac gcg ctg gtc atg ctc gcc ttc gtg gcg gat tcg agc 493

Val Leu Gly Asn Ala Leu Val Met Leu Ala Phe Val Ala Asp Ser Ser

50

55

60

ctc cgc acc cag aac aac ttc ttt ctg ctc aac ctc gcc atc tcc gac 541

Leu Arg Thr Gln Asn Asn Phe Phe Leu Leu Asn Leu Ala Ile Ser Asp

65

70

75

80

ttc ctc gtg ggt gcc ttc tgc atc cca ttg tac gta ccc tat gtg ctg 589

Phe Leu Val Gly Ala Phe Cys Ile Pro Leu Tyr Val Pro Tyr Val Leu

85

90

95

acc ggc cgt tgg acc ttc ggc cgg ggc ctc tgc aag ctg igg ctg gig 637

Thr Gly Arg Trp Thr Phe Gly Arg Gly Leu Cys Lys Leu Trp Leu Val

100

105

110

gta gac tac cta ctg tgc gcc tcc tcg gtc ttc aac atc gta ctc atc 685

Val Asp Tyr Leu Leu Cys Ala Ser Ser Val Phe Asn Ile Val Leu Ile

115

120

125

agc tat gac cga ttc ctg tca gtc act cga gct gtc tcc tac agg gcc 733

Ser Tyr Asp Arg Phe Leu Ser Val Thr Arg Ala Val Ser Tyr Arg Ala

130

135

140

cag cag ggg gac acg aga cgg gcc gtt cgg aag atg gca ctg gig tgg 781

Gln Gln Gly Asp Thr Arg Arg Ala Val Arg Lys Met Ala Leu Val Trp

145

150

155

160

gtg ctg gcc ttc ctg ctg tat ggg cct gcc atc ctg agt tgg gag tac 829

Val Leu Ala Phe Leu Leu Tyr Gly Pro Ala Ile Leu Ser Trp Glu Tyr

165

170

175

ctg tct ggt ggc agt tcc atc ccc gag ggc cac tgc tat gct gag ttc 877

Leu Ser Gly Gly Ser Ser Ile Pro Glu Gly His Cys Tyr Ala Glu Phe

180

185

190

ttc tac aac tgg tac ttt ctc atc acg gcc tcc acc ctc gag ttc ttc 925

Phe Tyr Asn Trp Tyr Phe Leu Ile Thr Ala Ser Thr Leu Glu Phe Phe

195	200	205
acg ccc ttc ctc agc gtt acc ttc ttc aac ctc agc atc tac ctg aac 973		
Thr Pro Phe Leu Ser Val Thr Phe Phe Asn Leu Ser Ile Tyr Leu Asn		
210	215	220
atc cag agg cgc acc cgc ctt cgg ctt gat ggg ggc cgt gag gct ggc 1021		
Ile Gln Arg Arg Thr Arg Leu Arg Leu Asp Gly Gly Arg Glu Ala Gly		
225	230	235
240		
cca gaa ccc cca cca gat gcc cag ccc tcg cca cct cca gct ccc ccc 1069		
Pro Glu Pro Pro Pro Asp Ala Gln Pro Ser Pro Pro Pro Ala Pro Pro		
245	250	255
agc tgc tgg ggc tgc tgg cca aaa ggg cat ggc gag gcc atg ccg ttg 1117		
Ser Cys Trp Gly Cys Trp Pro Lys Gly His Gly Glu Ala Met Pro Leu		
260	265	270
cac agg tat ggg gtg ggt gag gca ggc cct ggt gtt gag gct ggg gag 1165		
His Arg Tyr Gly Val Gly Glu Ala Gly Pro Gly Val Glu Ala Gly Glu		
275	280	285
gct gcc ctc ggg ggt ggc agt ggt gga ggt gct gct gcc tcg ccc acc 1213		
Ala Ala Leu Gly Gly Ser Gly Gly Ala Ala Ala Ser Pro Thr		
290	295	300

tcc agc tct ggc agc tcc tca agg ggc act gag agg cca cgc tca ctc 1261
 Ser Ser Ser Gly Ser Ser Arg Gly Thr Glu Arg Pro Arg Ser Leu
 305 310 315 320

aaa agg ggc tcc aag cca tca gca tct tca gca tcc ctg gag aag cgc 1309
 Lys Arg Gly Ser Lys Pro Ser Ala Ser Ser Ala Ser Leu Glu Lys Arg
 325 330 335

atg aag atg gtg tcc cag agc atc acc cag cgc ttc cgg ctg tcg cgg 1357
 Met Lys Met Val Ser Gln Ser Ile Thr Gln Arg Phe Arg Leu Ser Arg
 340 345 350

gac aag aag gig gcc aag tcg ctg gcc atc atc gtg agc atc tit ggg 1405
 Asp Lys Lys Val Ala Lys Ser Leu Ala Ile Ile Val Ser Ile Phe Gly
 355 360 365

ctc tgc tgg gcg ccg tac acg ctc cta atg atc atc cga gct gct tgc 1453
 Leu Cys Trp Ala Pro Tyr Thr Leu Leu Met Ile Ile Arg Ala Ala Cys
 370 375 380

cat ggc cgc tgc atc ccc gat tac tgg tac gag acg tcc ttc tgg ctt 1501
 His Gly Arg Cys Ile Pro Asp Tyr Trp Tyr Glu Thr Ser Phe Trp Leu
 385 390 395 400

ctg tgg gcc aac tcg gcc gtc aac ccc gtc ctc tac cca ctg tgc cac 1549
 Leu Trp Ala Asn Ser Ala Val Asn Pro Val Leu Tyr Pro Leu Cys His

